REMARKS

This document is submitted in response to the Office Action dated April 5, 2006 ("Office Action").

Claims 17, 22-23, 34, 42, 44, and 47 have been amended. Claims 48-51 have been newly added. Additionally, Applicant has canceled claims 43, and 45-46. Support for the amendment to independent claims 17 and 34 can be found in the Specification, e.g., at page 1, lines 23-24. Claim 42 has been amended to correct for the antecedent basis of a limitation. Claim 47 has been amended to correct for its dependency. Claims 22-23 and 34 have also been amended to more clearly set forth the claimed invention. Support for new claims 48-49, dependent from claim 17, and new claims 50-51, dependent from claim 34, is found in the Specification, e.g., at page 19, lines 20-26. No new matter is added.

Upon entry of the proposed amendments, claims 17-20, 22-35, 42, 44, and 47-51 will be under examination. Reconsideration of the application is respectfully requested in view of the remarks below.

Claim Objections

Claim 44 is objected to for a typographical error. See the Office Action, page 2, line 12. Applicant has amended claim 44 to delete the redundant "wherein the" as requested by the Examiner.

Claims 18, 20, 29-33, 44, and 46-47 are objected to as being dependent from rejected claims. See the Office Action, page 7, lines 1-2. Applicant submits that the grounds for the objections have been overcome for the reasons set forth below and requests that the objections be withdrawn.

Rejections under 35 U.S.C. § 112 second paragraph

Claim 42 is rejected as indefinite. See the Office Action, page 2, lines 17-19.

The Examiner pointed out that the phrase "the method of claim 20" in claim 42 lacks sufficient antecedent basis, given that claim 20 does not recite a method. See the Office Action,

page 3, lines 1-2. Applicants have amended claim 42 to recite "the method of claim 35", which has proper antecedent basis. Therefore, amended claim 42 is definite.

Rejections under 35 U.S.C. § 101

Claims 22-23, and 34 were rejected as directed toward non-statutory subject matter. See the Office Action, page 6, lines 11-12. The Examiner indicated that these claims recite "a cell," which reads on human. See the Office Action, page 6, line 13. Applicant has amended these claims to recite "an isolated cell" as suggested by the Examiner.

Rejections under 35 U.S.C. § 112 first paragraph (written description)

Claims 17, 19, 22, 24-28, 34-35, 43 and 45 were rejected for lacking written description. See the Office Action, page 3, lines 4-8.

Applicant has cancelled claims 43 and 45 and will discuss independent claim 17 first. Claim 17 covers a genus of nucleic acid molecules of at least 500 bases that hybridize to SEQ ID NO:1 or its complementary sequence under stringent conditions.

The Examiner, reiterating his grounds from the previous office action, asserted that Applicant does not describe a representative number of nucleic acid sequences to demonstrate possession of the genus of claim 17, as only one such sequence is disclosed. See the Office Action, page 3, lines 8-9; page 4, lines 5-7. The Examiner further asserted that the claim is not analogous to Example 9 of the written description guideline training material in that it "does not recite a specific molecular function that leads to a specific biochemical function or phenotypic change ..." See the Office Action, page 4, lines 7-9.

In the sole interest of moving this case toward allowance, Applicant has amended claim 17. Claim 17, as amended, covers a genus of isolated nucleic acid molecules that hybridize to SEQ ID NO:1 under stringent conditions and encode polypeptides capable of binding to DNA containing one or more copies of a TATCCA sequence. In view of the amendment, Applicant submits that the additional functional limitation renders the claim analogous to Example 9, and adequately narrows the claimed genus so that SEQ ID NO: 1 is representative of the genus.

The Examiner correctly pointed out that MYB proteins (i.e. OsMYBS1, OsMYBS2 and OsMYBS3) capable of binding to the TATCCA sequence may include both transcriptional activators and repressors. See the Office Action, page 4, lines 12-15. Applicant would like to point out that, given the teachings from the specification, a skilled person would expect these MYB proteins to possess different functions, since they share little amino acid or nucleic acid sequence homology. As stated in the Specification, "there is very little homology among the N- and C-terminal regions outside the 1R regions of all of the MYB proteins with 1R DNA-binding domains ..." See page 16, lines 21-24. The 1R region consists of only about 51 amino acids, thus is approximately 153 bases in length. See the Specification, page1, lines 12-13. In fact, sequence alignment shows that OsMYBS1 (SEQ ID NO: 1) and OsMYBS2 (SEQ ID NO:2) only share 72% sequence identity within a 165-bases segment out of more than 1000 bases. See Exhibit "A", page 1. Further, OsMYBS1 and OsMYBS3 (SEQ ID NO:3) share no significant sequence homology at all. See Exhibit "A", page 3. The functional diversity among MYB proteins is, therefore, inherently manifested within their sequence diversity. See Specification, page 1, line 12. Without significant sequence homology spanning their entire lengths, Applicant submits that two nucleic acid molecules are unlikely to hybridize to each other under stringent conditions. As the claimed genus of nucleic acid molecules must have at least 500 bases and hybridize to SEQ ID NO:1 under stringent conditions, a skilled person would expect them to share significant sequence homology with SEQ ID NO:1 beyond the 1R region, so that they would encode proteins having similar functions as that of OsMYBS1.

In view of the above amendments and remarks, Applicant submits that, like the claim in Example 9, amended claim 17 covers a narrow genus of nucleic acid molecules encoding proteins with a specific function, so that a skilled person would not expect substantial variation within the genus. SEQ ID NO: 1 is hence, contrary to the Examiner's assertion, representative of the claimed genus.

Based on the foregoing remarks, amended claim 17 satisfies the written description requirement under 35 U.S.C. § 112. As claims 19, 22, 24-28, and new claims 48-49 depend either directly or indirectly from claim 17, they are also adequately described for at least the

same reasons. Further, amended independent claim 34, as well as claim 35 and new claims 50-51 cover a narrow genus of nucleic acid molecules encoding proteins that bind the TATCCA sequence, so are also adequately described for at least the same reasons set forth above.

Rejections under 35 U.S.C. § 112 first paragraph (enablement)

Claims 17, 19, 22, 24-28, 34-35, 43, and 45 were rejected as lacking enablement. See the Office Action, page 4, lines 17-18. Claims 43 and 45 have been canceled.

Applicant will again discuss independent claim 17 first. The Examiner, maintaining the grounds raised in the previous office action, contended that claim 17 covers a number of nucleic acid molecules encoding proteins with activities different from that of OsMYBS1, so that it would require undue experimentation for a skilled person to make the claimed nucleic acid molecules. See the Office Action, page 5, lines 11-15.

As discussed above, amended claim 17 covers a narrow genus of nucleic acid molecules encoding proteins capable of binding to DNA containing one or more copies of a TATCCA sequence. Given the small number of structurally similar nucleic acid molecules encompassed by claim 17 and that the Specification teaches methods of assaying for the required binding activity, a skilled person would not have to perform undue experimentation to make the claimed nucleic acid molecule.

Therefore, Applicants submit that amended claim 17 is enabled under 35 U.S.C. § 112. As claims 19, 22, 24-28, and new claims 48-49 depend either directly or indirectly from claim 17, they are enabled for at least the same reasons. Additionally, amended independent claim 34, as well as claim 35 and new claims 50-51, cover a narrow genus of nucleic acid molecules encoding proteins that bind the TATCCA sequence, so are also enabled for at least the same reasons set forth above.

CONCLUSION

Applicant submits that the grounds for the rejections and objections asserted in the Office Action have been overcome. All pending claims under examinations are patentable. Thus, allowance of this application is proper, and early favorable action is respectfully solicited.

Enclosed is a Petition for One Month Extension of Time. The extension fee in the amount of $60 is being paid concurrently on the Electronic Filing System (EFS) by way of Deposit Account authorization. Please apply any other required fees to deposit account 06 1050, referencing the attorney docket number shown above.

Respectfully submitted,

Date: 8-7-2006

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EXHIBIT A

Exhibit A

Nucleic Acid Sequence Alignment : SEQ ID NO:1 vs. SEQ ID NO: 2

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.14 [May-07-2006]

Match: 1 Mismatch: -2 gap open: 5 gap extension: 2
x_dropoff: 50 expect: 10.00 wordsize: 11 Filter View option Standard
Masking character option X for protein, n for nucleotide Masking color option Black
Show CDS translation

Sequence 1: lcl|1_seq_1 **(SEQ ID NO: 1)**
Length = 1330 (1 .. 1330)

Sequence 2: lcl|2_seq_2 **(SEQ ID NO: 2)**
Length = 1012 (1 .. 1012)

```
 Score = 58.4 bits (30),  Expect = 6e-05
 Identities = 120/165 (72%), Gaps = 0/165 (0%)
 Strand=Plus/Plus

Query  424  GCAGGAGAGGCGCAAGGGCATCCCATGGACGGAGGAAGAGCACAGGCTGTTCTTGCTGGG  483
            ||||||||||    || ||  | |||||||| ||||| |||||||  |   ||| ||   ||
Sbjct  208  GCAGGAGAGGAAGAAAGGGGTACCATGGACTGAGGAGGAGCACAAGAAATTCCTGGAAGG  267

Query  484  GCTGGACAAGTTCGGCAAGGGGGACTGGCGGAGCATCTCGCGCAACTTCGTCATCTCGCG  543
            ||||    || | || || ||||||||| |  |||||||    ||||| || | |    |
Sbjct  268  GCTGAGGCAGCTGGGGAAAGGGGACTGGAGAGGCATCTCCAAGAACTTTGTGACCAGCAG  327

Query  544  GACGCCAACGCAGGTGGCGAGCCACGCGCAGAAGTACTTCATCCG  588
            |||| | || |||||||| |||||||| |||||||||||| ||||
Sbjct  328  GACGGCGACTCAGGTGGCCAGCCACGCCCAGAAGTACTTCCTCCG  372


CPU time:      0.01 user secs.      0.00 sys. secs          0.01 total secs.

Lambda     K      H
    1.33    0.621     1.12

Gapped
Lambda     K      H
    1.33    0.621     1.12

Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 5, Extension: 2
Number of Sequences: 1
Number of Hits to DB: 37
Number of extensions: 7
Number of successful extensions: 3
Number of sequences better than 10.0: 1
Number of HSP's gapped: 3
Number of HSP's successfully gapped: 1
```

```
Length of query: 1330
Length of database: 17,869,364,704
Length adjustment: 26
Effective length of query: 1304
Effective length of database: 17,869,364,678
Effective search space: 23301651540112
Effective search space used: 23301651540112
X1: 11 (21.1 bits)
X2: 26 (50.0 bits)
X3: 26 (50.0 bits)
S1: 13 (25.7 bits)
S2: 22 (43.0 bits)
```

Nucleic Acid Sequence Alignment : SEQ ID NO:1 vs. SEQ ID NO: 3

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.14 [May-07-2006]

Match: 1 Mismatch: -2 gap open: 5 gap extension: 2
x_dropoff: 50 expect: 10.0 wordsize: 11 Filter View option Standard
Masking character option X for protein, n for nucleotide Masking color option Black
Show CDS translation

Sequence 1: lcl|1_seq_1
Length = 1330

Sequence 2: lcl|2_seq_2
Length = 1287

No significant similarity was found

```
CPU time:      0.01 user secs.      0.00 sys. secs          0.01 total secs.

Lambda      K       H
    1.33    0.621     1.12

Gapped
Lambda      K       H
    1.33    0.621     1.12


Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 5, Extension: 2
Number of Sequences: 1
Number of Hits to DB: 33
Number of extensions: 1
Number of sequences better than 10.0: 0
Number of HSP's gapped: 0
Number of HSP's successfully gapped: 0
Length of query: 1330
Length of database: 17,869,364,704
Length adjustment: 26
Effective length of query: 1304
Effective length of database: 17,869,364,678
Effective search space: 23301651540112
Effective search space used: 23301651540112
X1: 11 (21.1 bits)
X2: 26 (50.0 bits)
X3: 26 (50.0 bits)
S1: 13 (25.7 bits)
S2: 22 (43.0 bits)
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